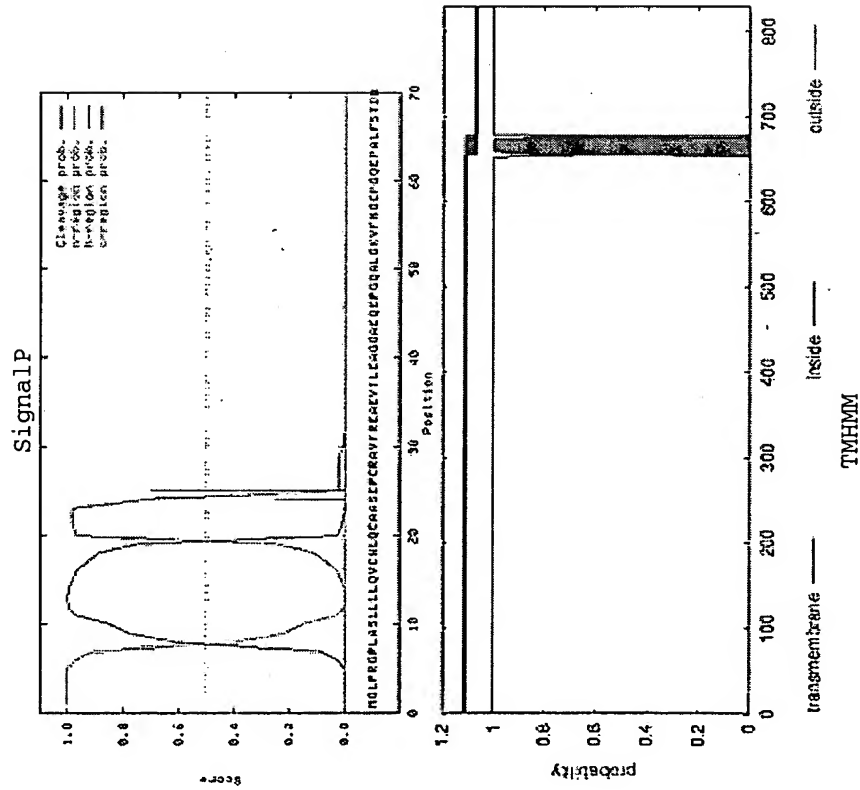


**Figure 1**

**PCTUC5 829 amino acids**

ANALYSIS  
 Cleaved signal peptide  
 Cleavage site = between position 24 and 25  
 MGLPRGPLASLLLLLQVCWLQCAAS ↓ EPCRAVFREA...  
 Topology  
 N-terminus external & C-terminus internal  
 residues 25 - 654 = extracellular  
 residues 655 - 677 = transmembrane  
 residues 678 - 829 = intracellular

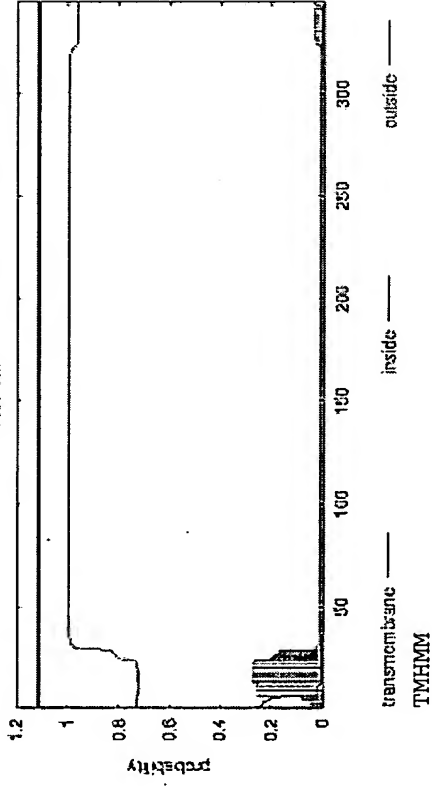
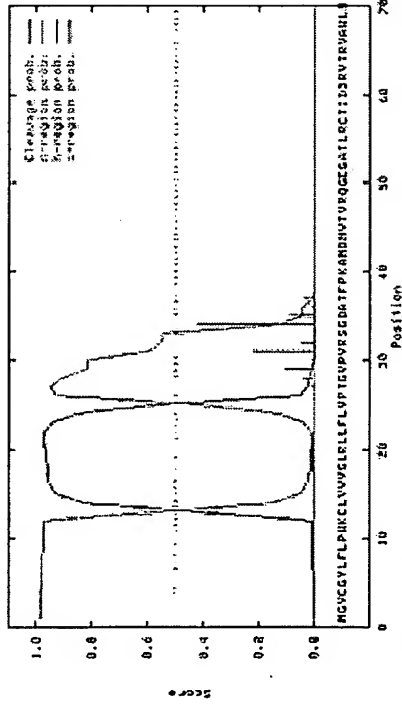


RESULTS  
 signal peptide probability > 99.9%  
 maximum cleavage site probability = 70.2%  
 number of probable transmembrane regions = 1

Figure 2

PCTUC93 345 amino acids

SignalP



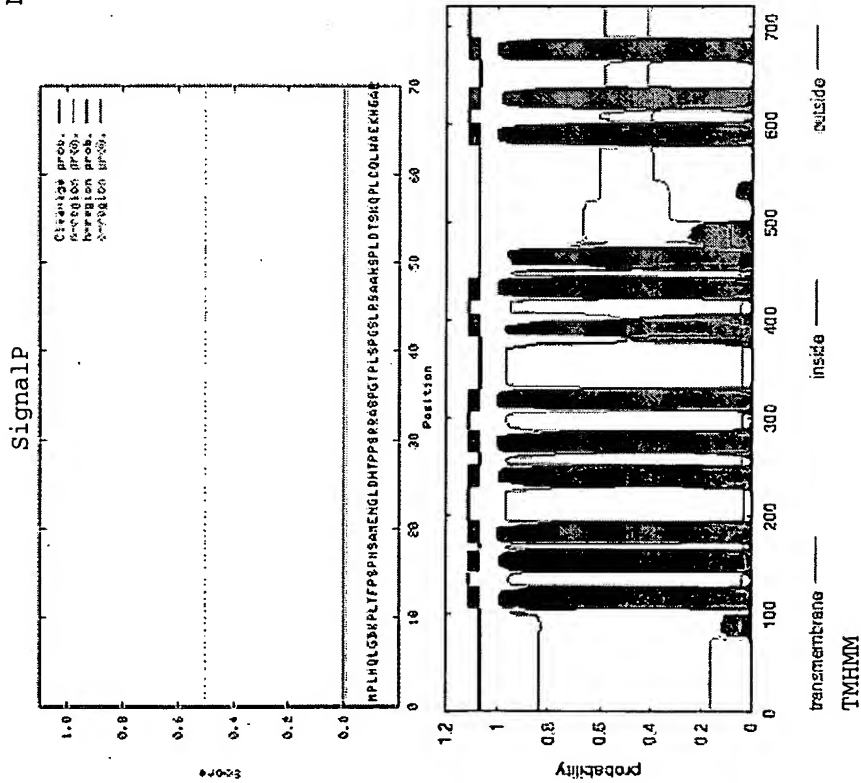
RESULTS  
signal peptide probability = 98.3%  
maximum cleavage site probability = 41.9%  
number of probable transmembrane regions = 0

ANALYSIS  
Cleaved signal peptide  
Cleavage site = between position 33 and 34  
MGVCGYLFPLPWKCLVVVSLRLLFLVPTGVPVRS ↓  
GDATFPKAMD...

Topology  
\*SECRETED\*  
residues 34 - 345 = extracellular

Figure 3

PCTUC190 722 amino acids



ANALYSIS

N-terminal signal sequence independent membrane insertion

Topology

N-terminus internal & C-terminus external

residues 1 - 105 = intracellular  
residues 106 - 128 = transmembrane  
residues 129 - 142 = extracellular  
residues 143 - 165 = transmembrane  
residues 166 - 171 = intracellular  
residues 172 - 194 = transmembrane  
residues 195 - 229 = extracellular  
residues 230 - 252 = transmembrane  
residues 253 - 264 = intracellular  
residues 265 - 287 = transmembrane  
residues 288 - 306 = extracellular  
residues 307 - 329 = transmembrane  
residues 330 - 383 = intracellular  
residues 384 - 406 = transmembrane  
residues 407 - 420 = extracellular  
residues 421 - 443 = transmembrane  
residues 444 - 578 = intracellular  
residues 579 - 601 = transmembrane  
residues 602 - 615 = extracellular  
residues 616 - 638 = transmembrane  
residues 639 - 666 = intracellular  
residues 667 - 689 = transmembrane  
residues 690 - 722 = extracellular

RESULTS

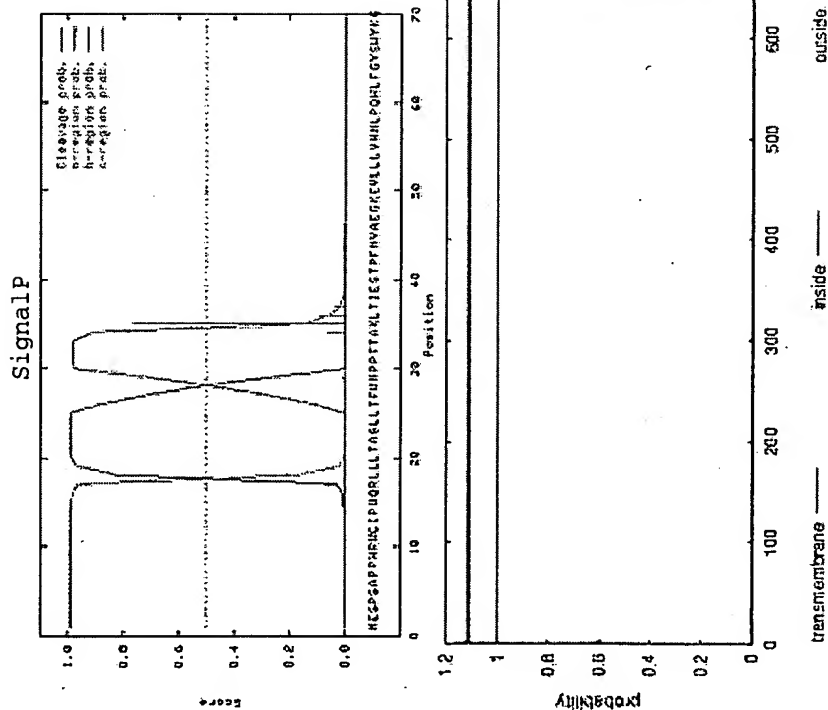
signal peptide probability = 0%

signal anchor probability = 0%

number of probable transmembrane regions =

Figure 4

PCTUC239 702 amino acids



TMHMM

ANALYSIS

Cleaved signal peptide

Cleavage site = between position 34 and 35

MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTA ↓

KLTISTPFN...

Topology

\*SECRETED\*

residues 35 - 702 = extracellular

RESULTS

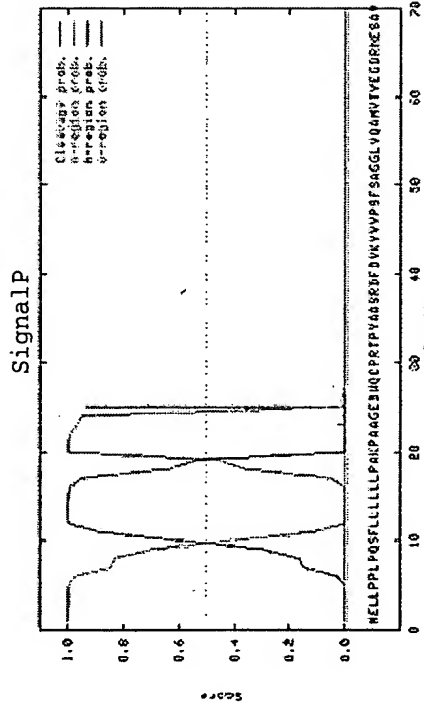
signal peptide probability = 99.3%

maximum cleavage site probability = 76.5%

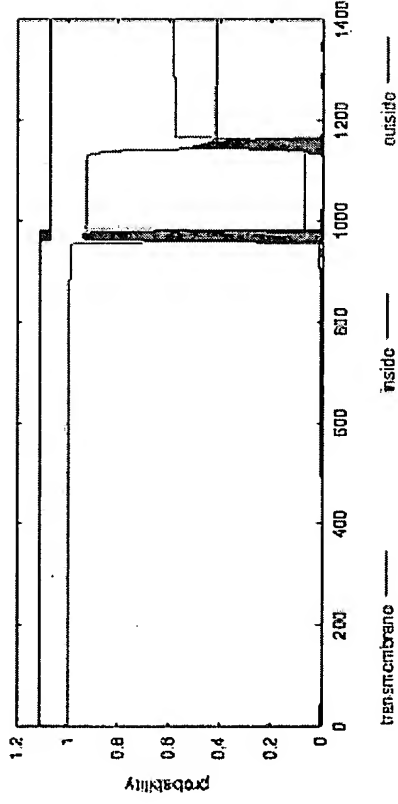
number of probable transmembrane regions = 0

**Figure 5**

**PCTUC246** 1400 amino acids



ANALYSIS  
 Cleaved signal peptide  
 Cleavage site = between position 24 and 25  
 MELLPLPQSFLLLLLLPAKPAAG ↓ EDWQCPRTPY...  
 Topology  
 N-terminus external & C-terminus internal  
 residues 25 - 959 = extracellular  
 residues 960 - 982 = transmembrane  
 residues 983 -1400 = intracellular

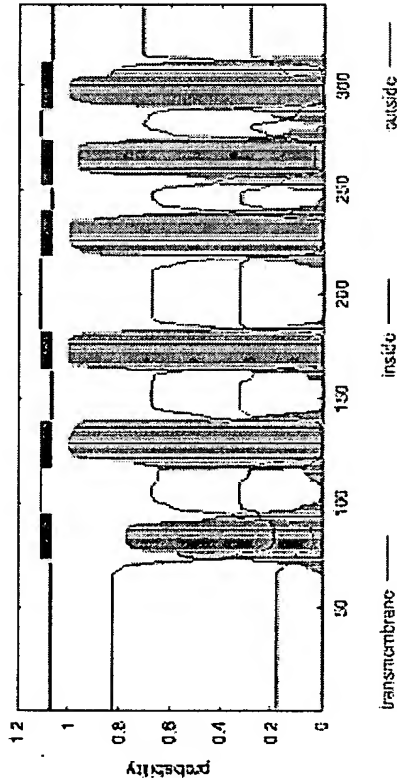
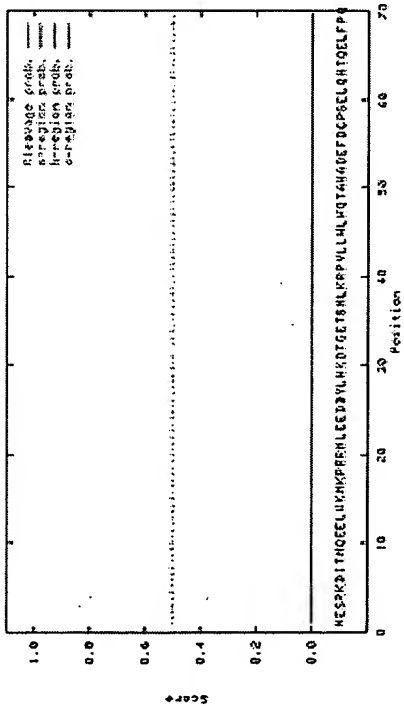


RESULTS  
 signal peptide probability > 99.9%  
 maximum cleavage site probability = 93.6%  
 number of probable transmembrane regions = 1

Figure 6

PCTUC360 339 amino acids

SignalP



TMHMM

RESULTS

signal peptide probability = 0%  
signal anchor probability = 0%  
number of probable transmembrane regions = 6

ANALYSIS

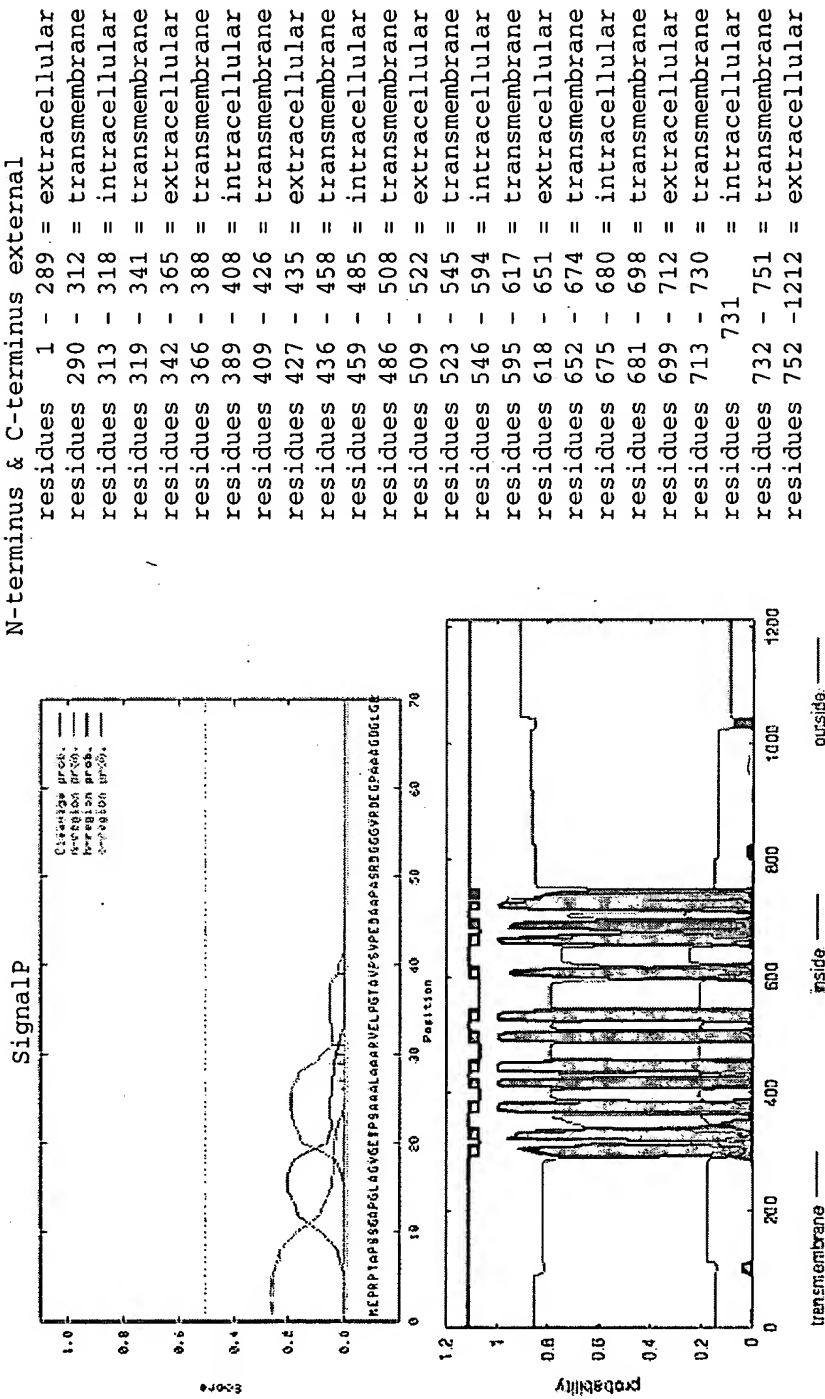
N-terminal signal sequence independent membrane insertion  
Topology

N-terminus & C-terminus internal

residues 1 - 72 = intracellular  
residues 73 - 95 = transmembrane  
residues 96 - 116 = extracellular  
residues 117 - 139 = transmembrane  
residues 140 - 163 = intracellular  
residues 164 - 182 = transmembrane  
residues 183 - 217 = extracellular  
residues 218 - 240 = transmembrane  
residues 241 - 251 = intracellular  
residues 252 - 274 = transmembrane  
residues 275 - 288 = extracellular  
residues 289 - 311 = transmembrane  
residues 312 - 339 = intracellular

Figure 7

PCTUC462 1212 amino acids



TMHMM

RESULTS

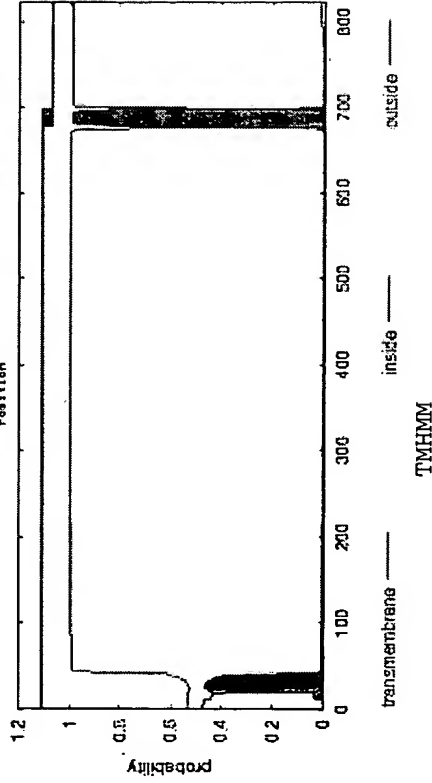
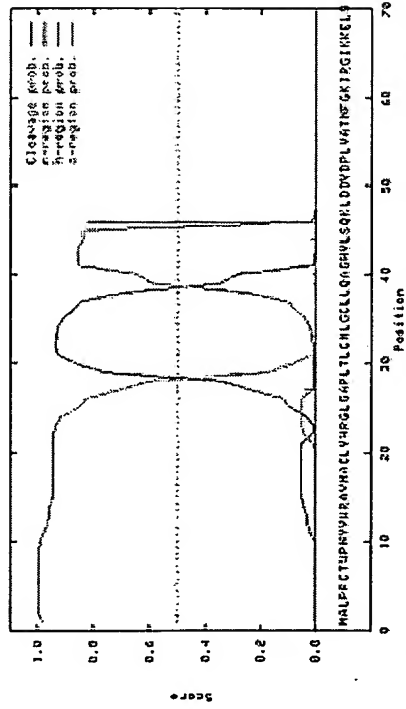
signal peptide probability = 25.9%  
 signal anchor probability = 0%  
 number of probable transmembrane regions = 12

**Figure 8**

**PCTUC468 823 amino acids**

ANALYSIS  
 Cleaved signal peptide  
 Cleavage site = between position 45 and 46  
 MALPRCTWPNYVVRVAVMACLVHRGLGAPLTLCMLGCLLQAGHVLS ↓  
 QKLDDVDPLV...  
 Topology  
 N-terminus external & C-terminus internal  
 residues 46 - 676 = extracellular  
 residues 677 - 699 = transmembrane  
 residues 700 - 823 = intracellular

**SignalP**



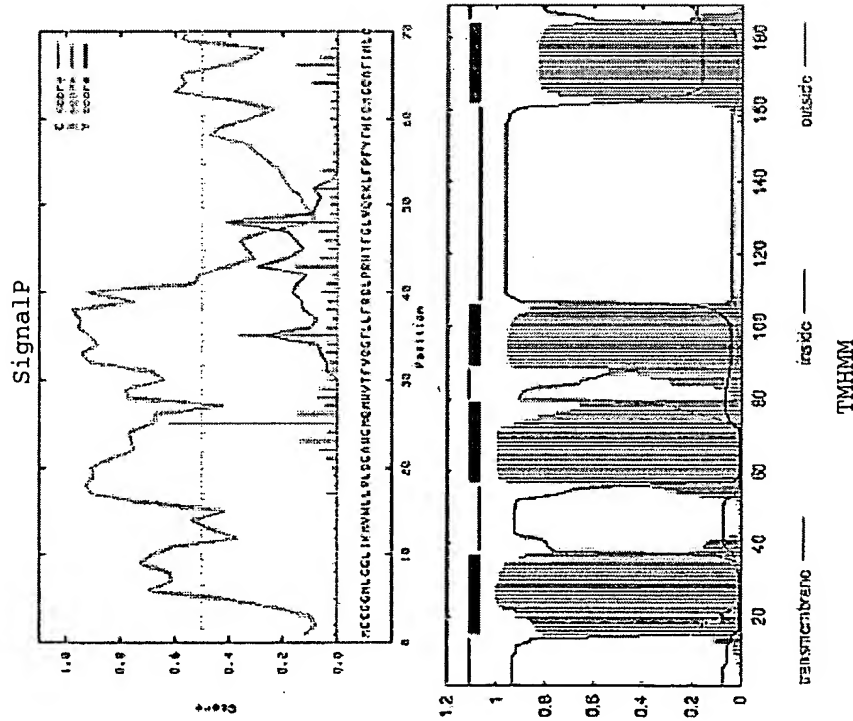
**RESULTS**

signal peptide probability = 98.4%  
 maximum cleavage site probability = 82.2%  
 number of probable transmembrane regions = 1



**Figure 9**

**PCTUC536 189 amino acids**



ANALYSIS  
Signal Anchor (non-cleaved signal peptide)  
Topology

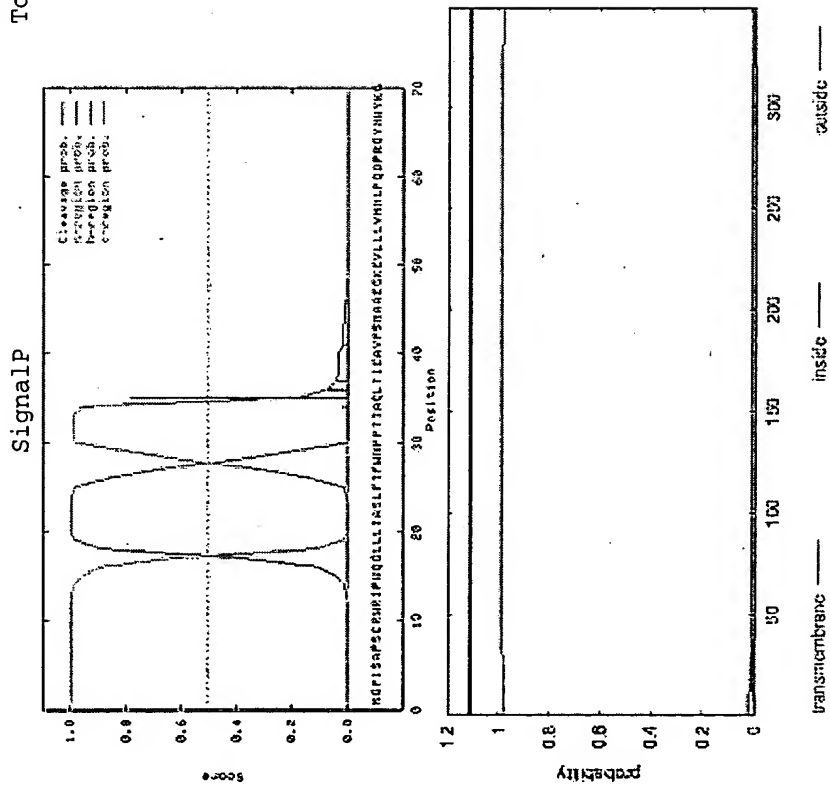
N-terminus & C-terminus external  
residues 1 - 14 = extracellular  
residues 15 - 37 = transmembrane  
residues 38 - 56 = intracellular  
residues 57 - 79 = transmembrane  
residues 80 - 88 = extracellular  
residues 89 - 106 = transmembrane  
residues 107 - 161 = intracellular  
residues 162 - 184 = transmembrane  
residues 185 - 189 = extracellular

RESULTS  
signal peptide probability = 29.2%  
signal anchor probability = 37.2%  
number of probable transmembrane regions = 4

**Figure 10**

**PCTUC582 349 amino acids**

ANALYSIS  
 Cleaved signal peptide  
 Cleavage site = between position 34 and 35  
 MGPI SAPSCRWRIPWQGLLTASLFTFWNPPTTA ↓  
 QLTIEAVPSN...  
 Topology  
 \*SECRETED\*  
 residues 35 - 349 = extracellular



TMHMM

# RESULTS

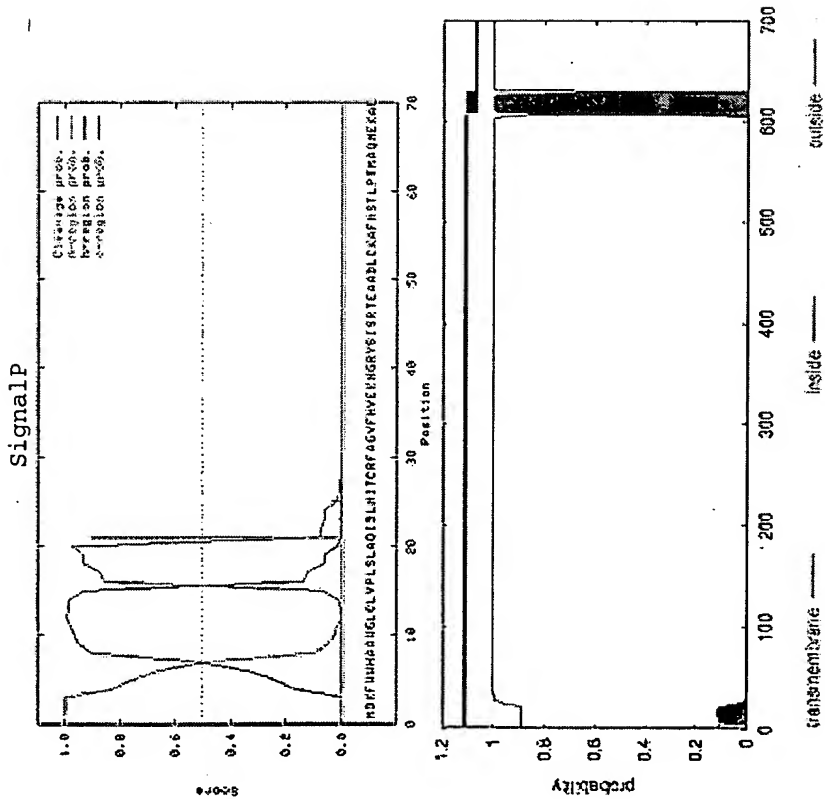
signal peptide probability = 99.3%  
 maximum cleavage site probability = 78.6%  
 number of probable transmembrane regions = 0

Figure 11

PCTUC605 699 amino acids

N-terminus external & C-terminus internal  
 residues 21 - 606 = extracellular  
 residues 607 - 629 = transmembrane  
 residues 630 - 699 = intracellular

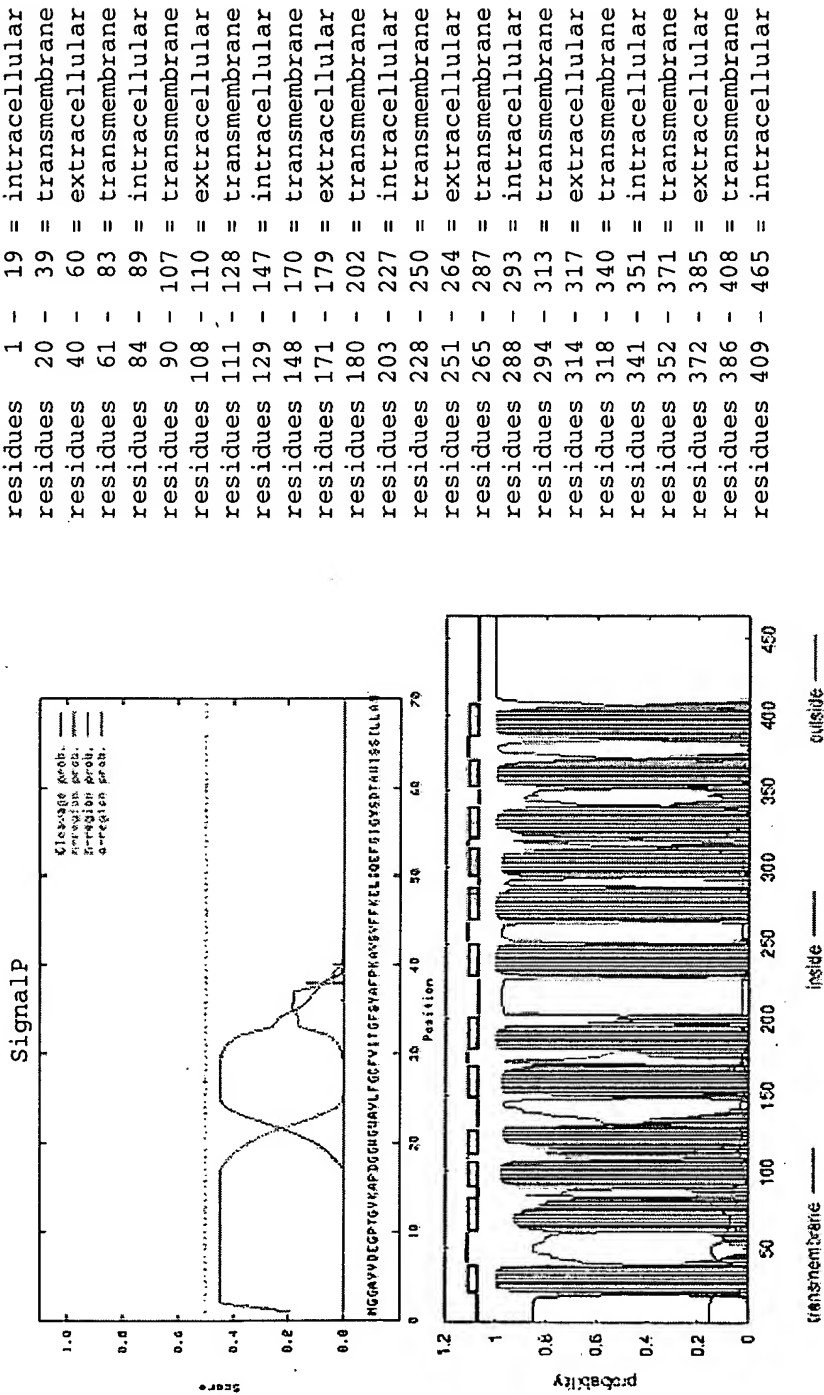
ANALYSIS  
 Cleaved signal peptide  
 Cleavage site = between position 20 and 21  
 MDKFWWFAAWGLCLVPLSLA ↓ QIDLNITCRF...  
 Topology



RESULTS  
 signal peptide probability = 99.7%  
 maximum cleavage site probability = 90.9%  
 number of probable transmembrane regions = 1

Figure 12

PCTUC629 465 amino acids



RESULTS

signal peptide probability = 19.3%  
 signal anchor probability = 25.6%  
 number of probable transmembrane regions = 12

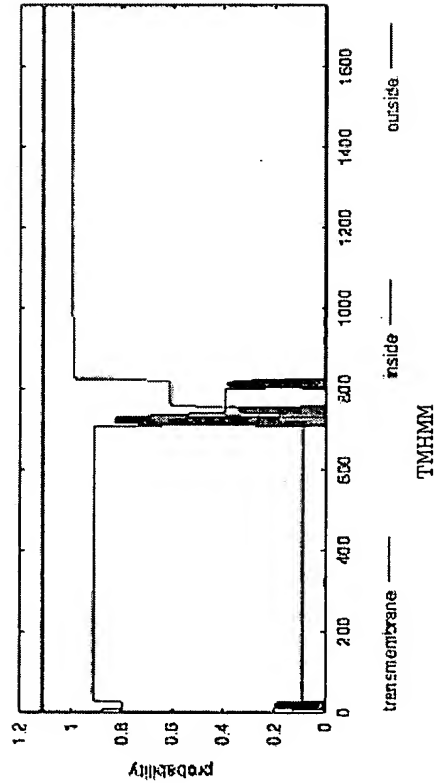
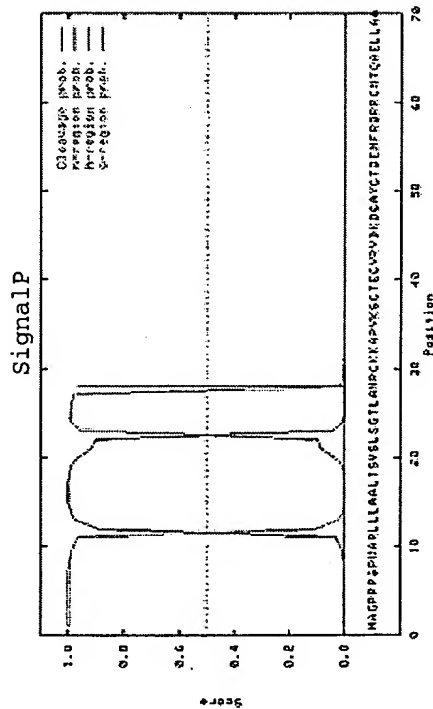
ANALYSIS  
 N-terminal signal sequence independent membrane insertion  
 Topology  
 N-terminus & C-terminus internal

residues 1 - 19 = intracellular  
 residues 20 - 39 = transmembrane  
 residues 40 - 60 = extracellular  
 residues 61 - 83 = transmembrane  
 residues 84 - 89 = intracellular  
 residues 90 - 107 = transmembrane  
 residues 108 - 110 = extracellular  
 residues 111 - 128 = transmembrane  
 residues 129 - 147 = intracellular  
 residues 148 - 170 = transmembrane  
 residues 171 - 179 = extracellular  
 residues 180 - 202 = transmembrane  
 residues 203 - 227 = intracellular  
 residues 228 - 250 = transmembrane  
 residues 251 - 264 = extracellular  
 residues 265 - 287 = transmembrane  
 residues 288 - 293 = intracellular  
 residues 294 - 313 = transmembrane  
 residues 314 - 317 = extracellular  
 residues 318 - 340 = transmembrane  
 residues 341 - 351 = intracellular  
 residues 352 - 371 = transmembrane  
 residues 372 - 385 = extracellular  
 residues 386 - 408 = transmembrane  
 residues 409 - 465 = intracellular

**Figure 13**

**PCTUC722 1752 amino acids**

ANALYSIS  
 Cleaved signal peptide  
 Cleavage site = between position 27 and 28  
 MAGPRPSPWARLLLAALISVLSGTLA ↓ NRCKKAPVKS...  
 Topology  
 \*SECRETED\*  
 residues 28 - 1752 = extracellular

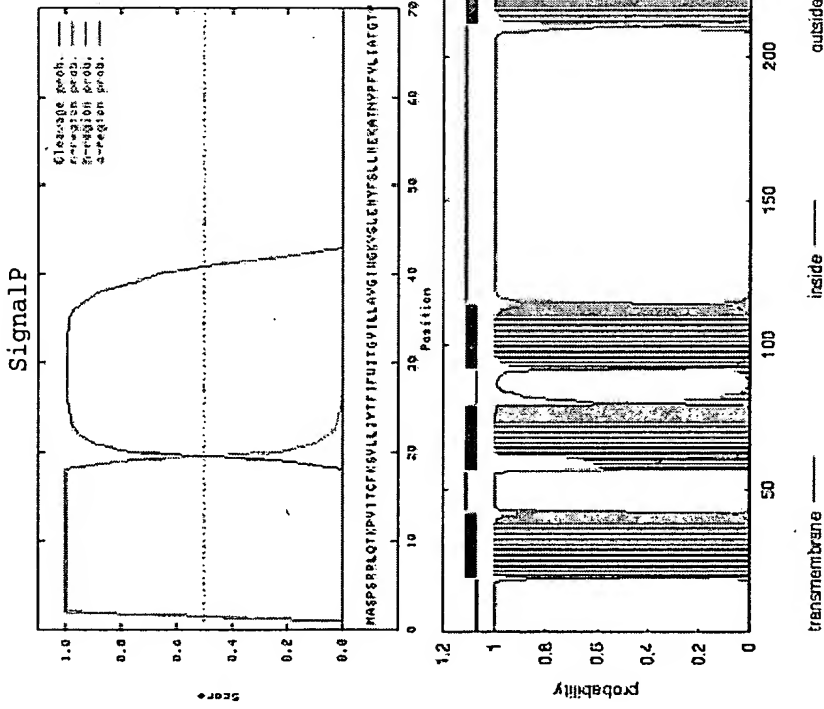


**RESULTS**

signal peptide probability > 99.9%  
 maximum cleavage site probability = 96.8%  
 number of probable transmembrane regions = 0

Figure 14

PCTUC748 245 amino acids



ANALYSIS  
Signal Anchor (non-cleaved signal peptide)  
Topology

N-terminus & C-terminus internal

residues 1 - 19 = intracellular  
residues 20 - 42 = transmembrane  
residues 43 - 56 = extracellular  
residues 57 - 79 = transmembrane  
residues 80 - 91 = intracellular  
residues 92 - 114 = transmembrane  
residues 115 - 210 = extracellular  
residues 211 - 233 = transmembrane  
residues 234 - 245 = intracellular

RESULTS

signal peptide probability = 0.3%

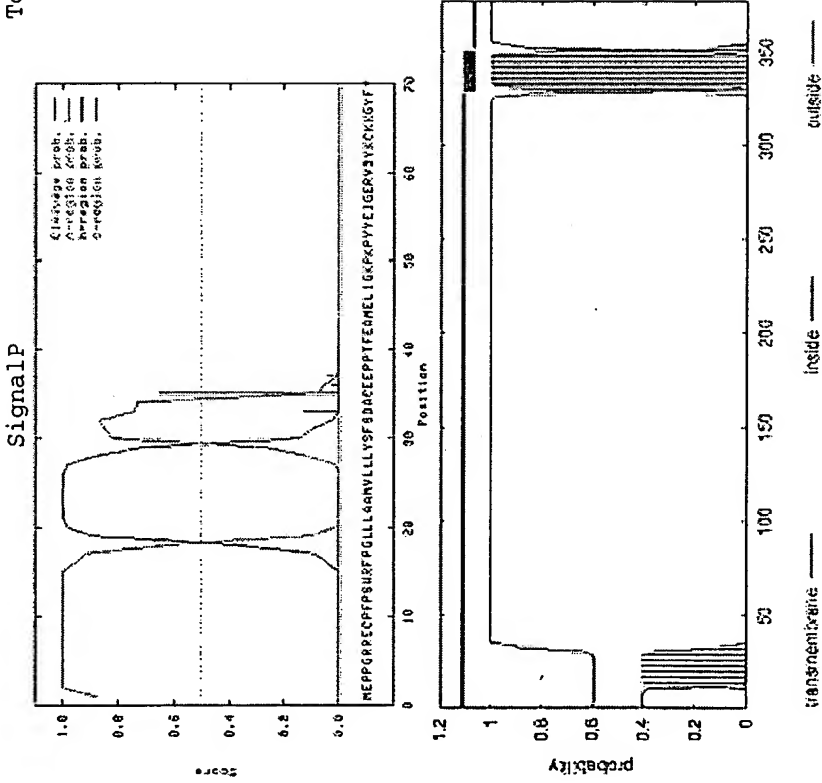
signal anchor probability = 99.7%

number of probable transmembrane regions = 4

Figure 15

PCTUC784 377 amino acids

ANALYSIS  
Cleaved signal peptide  
Cleavage site = between position 34 and 35  
MEPPGRRECFFPSWRFPGLLLAAMVLLLYSFSDA ↓  
CEEPTFEAM...  
Topology  
N-terminus external & C-terminus internal  
residues 35 - 328 = extracellular  
residues 329 - 351 = transmembrane  
residues 352 - 377 = intracellular



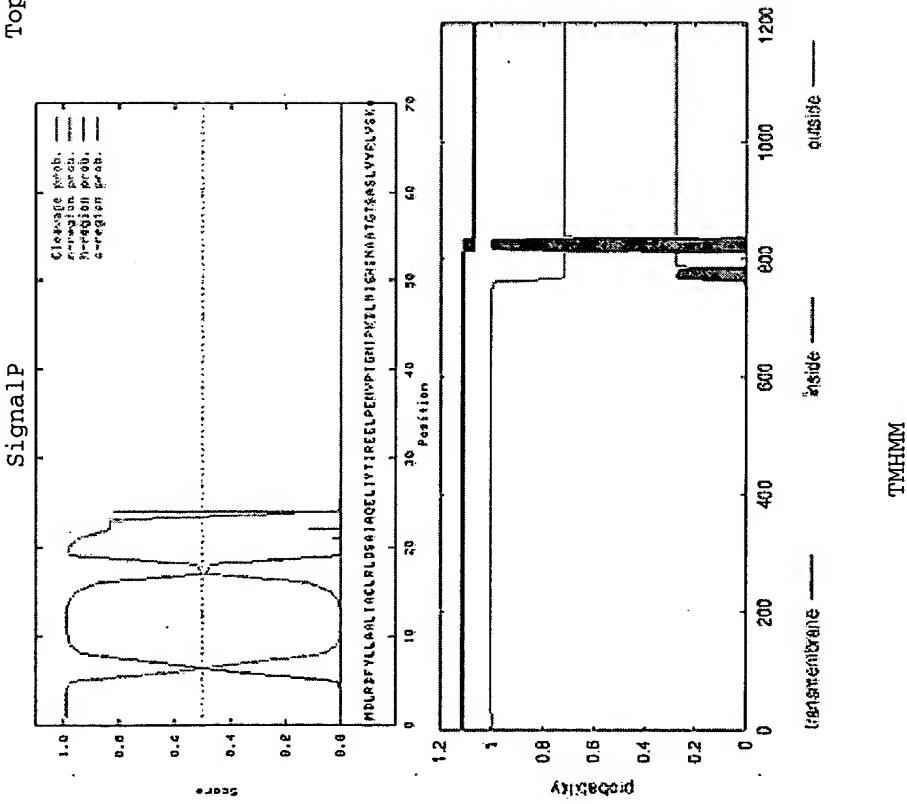
TMHMM

RESULTS  
signal peptide probability = 87.0%  
maximum cleavage site probability = 65.3%  
number of probable transmembrane regions = 1

Figure 16

PCTUC812 1203 amino acids

ANALYSIS  
Cleaved signal peptide  
Cleavage site = between position 23 and 24  
MDLRDFYLLAALIACLRLDSAIA ↓ QELIYTIREE...  
Topology  
N-terminus external & C-terminus internal  
residues 25 - 813 = extracellular  
residues 814 - 836 = transmembrane  
residues 837 -1203 = intracellular

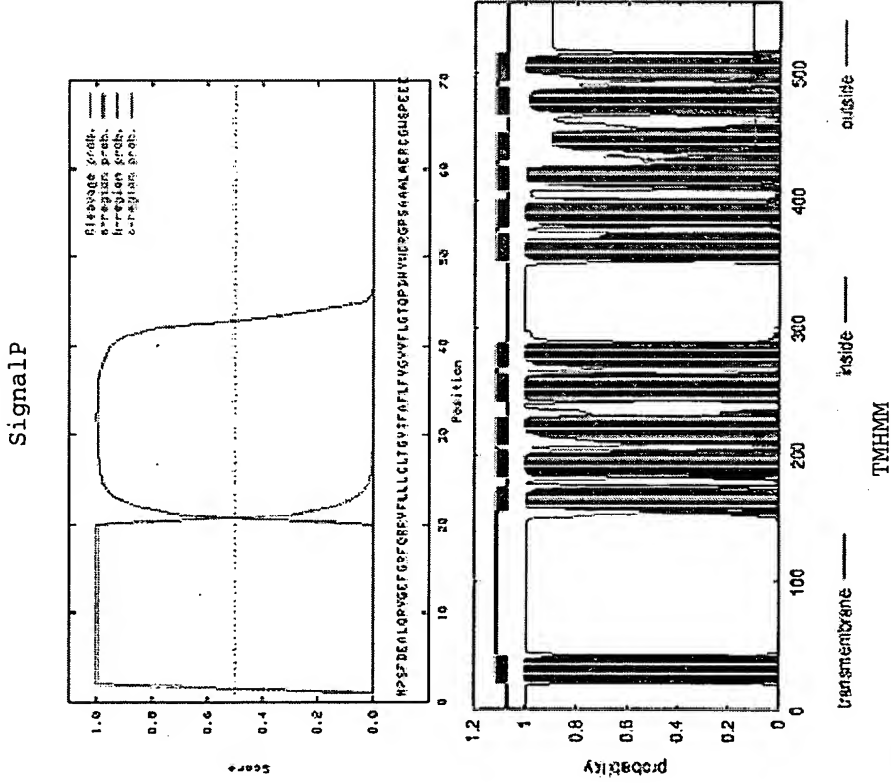


RESULTS  
signal peptide probability = 99.1%  
maximum cleavage site probability = 82.5%  
number of probable transmembrane regions = 1



Figure 17

PCTUC856 556 amino acids



RESULTS

signal peptide probability = 0.1%  
signal anchor probability = 99.9%  
number of probable transmembrane regions = 12

ANALYSIS

Signal Anchor (non-cleaved signal peptide)  
Topology

N-terminus & C-terminus internal

residues 1 - 20 = intracellular  
residues 21 - 43 = transmembrane  
residues 44 - 155 = extracellular  
residues 156 - 175 = transmembrane  
residues 176 - 181 = intracellular  
residues 182 - 204 = transmembrane  
residues 205 - 207 = extracellular  
residues 208 - 230 = transmembrane  
residues 231 - 241 = intracellular  
residues 242 - 264 = transmembrane  
residues 265 - 268 = extracellular  
residues 269 - 288 = transmembrane  
residues 289 - 351 = intracellular  
residues 352 - 374 = transmembrane  
residues 375 - 378 = extracellular  
residues 379 - 401 = transmembrane  
residues 402 - 407 = intracellular  
residues 408 - 427 = transmembrane  
residues 428 - 431 = extracellular  
residues 432 - 454 = transmembrane  
residues 455 - 466 = intracellular  
residues 467 - 489 = transmembrane  
residues 490 - 493 = extracellular  
residues 494 - 516 = transmembrane  
residues 517 - 556 = intracellular

Figure 18

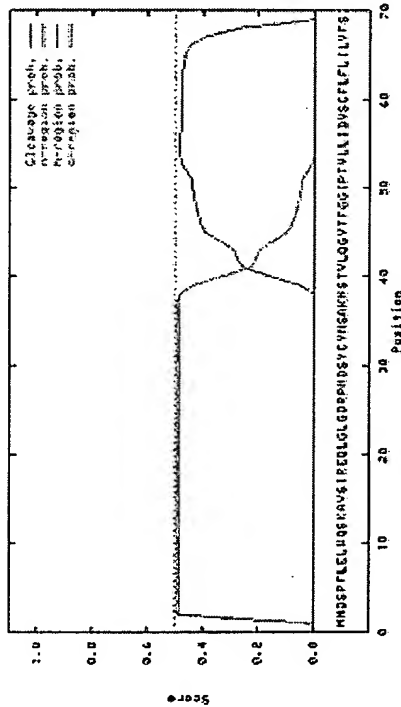
PCTUC898

807 amino acids

RESULTS

signal peptide probability = 0%  
signal anchor probability = 48.6%  
number of probable transmembrane regions = 10

SignalP



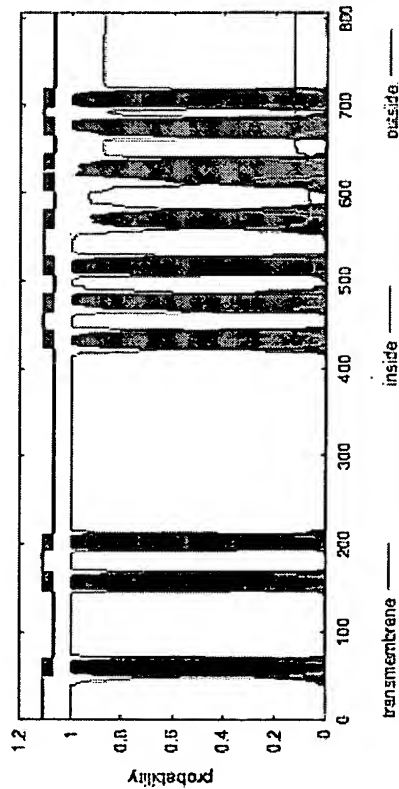
ANALYSIS

Signal Anchor (non-cleaved signal peptide)

Topology

N-terminus external & C-terminus internal

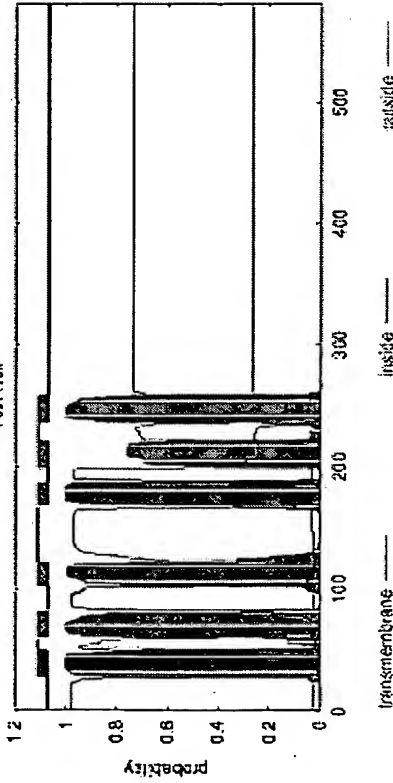
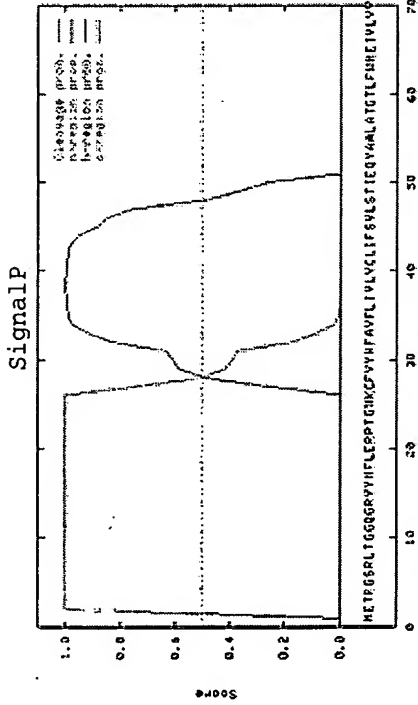
residues 1 - 48 = extracellular  
residues 49 - 71 = transmembrane  
residues 72 - 145 = intracellular  
residues 146 - 168 = transmembrane  
residues 169 - 191 = extracellular  
residues 192 - 211 = transmembrane  
residues 212 - 421 = intracellular  
residues 422 - 443 = transmembrane  
residues 444 - 462 = extracellular  
residues 463 - 485 = transmembrane  
residues 486 - 505 = intracellular  
residues 506 - 528 = transmembrane  
residues 529 - 558 = extracellular  
residues 559 - 581 = transmembrane  
residues 582 - 601 = intracellular  
residues 602 - 624 = transmembrane  
residues 625 - 627 = extracellular  
residues 628 - 645 = transmembrane  
residues 646 - 665 = intracellular  
residues 666 - 688 = transmembrane  
residues 689 - 697 = extracellular  
residues 698 - 720 = transmembrane  
residues 721 - 807 = intracellular



TMHMM

Figure 19

PCTUC935 581 amino acids



TMHMM

RESULTS

signal peptide probability = 0.02%

signal anchor probability = 99.8%

number of probable transmembrane regions = 6

ANALYSIS

Signal Anchor (non-cleaved signal peptide)

Topology

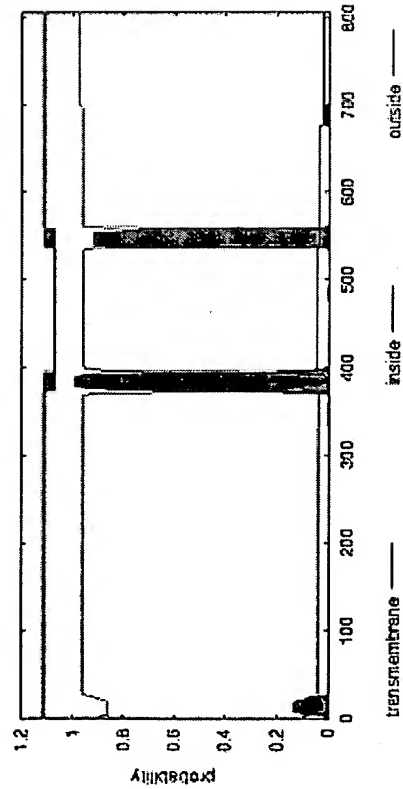
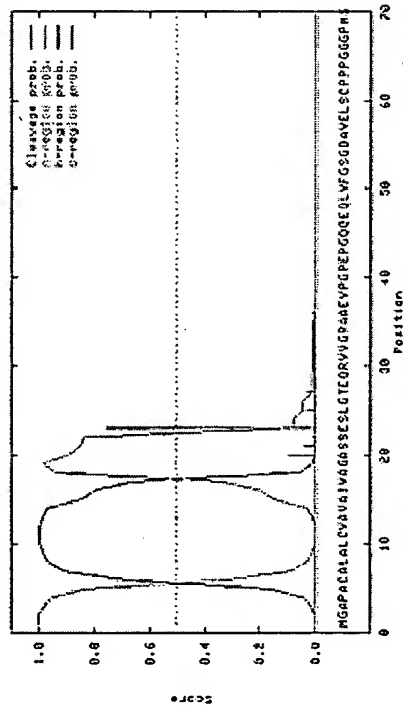
N-terminus & C-terminus internal  
residues 1 - 27 = intracellular  
residues 28 - 50 = transmembrane  
residues 51 - 59 = extracellular  
residues 60 - 82 = transmembrane  
residues 83 - 102 = intracellular  
residues 103 - 122 = transmembrane  
residues 123 - 167 = extracellular  
residues 168 - 187 = transmembrane  
residues 222 - 235 = extracellular  
residues 188 - 198 = intracellular  
residues 236 - 258 = transmembrane  
residues 199 - 221 = transmembrane  
residues 259 - 581 = intracellular

Figure 20

PCTUC936

806 amino acids

SignalP



TMHMM

# RESULTS

signal peptide probability > 99.9%

maximum cleavage site probability = 75.4%

number of probable transmembrane regions = 2

EXPERIMENTAL EVIDENCE SUPPORTS ONLY TM#1 REGION

## ANALYSIS

Cleaved signal peptide

Cleavage site = between position 22 and 23

MGAPACALALCVAVAIIVAGASS ↓ ESLGTEQRVV...

## Topology

N-terminus external & C-terminus internal

residues 24 - 372 = extracellular

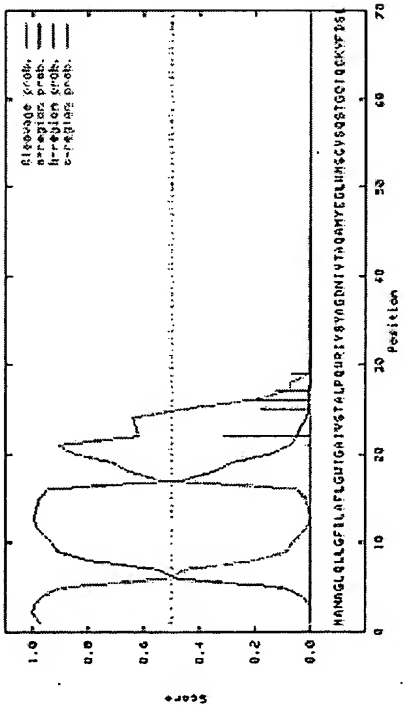
residues 373 - 395 = transmembrane

residues 396 - 806 = intracellular

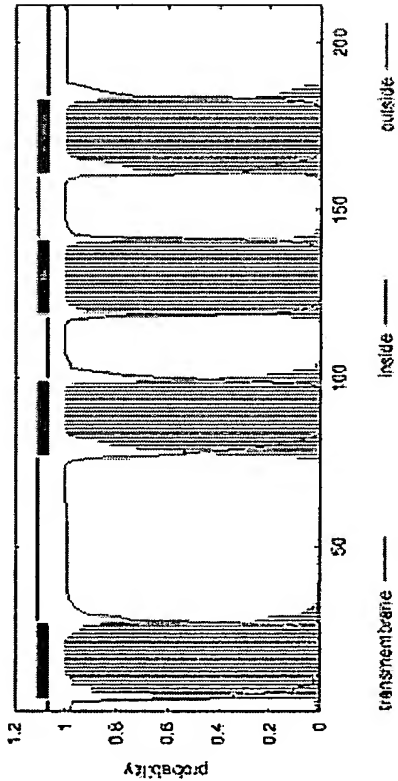
Figure 21

PCTUC986 211 amino acids

SignalP



ANALYSIS  
Cleaved signal peptide  
Cleavage site = between position 21 and 22  
MANAGLQLLGFIILFLGWIGAVSTALPQWR...  
Topology  
N-terminus external & C-terminus internal  
residues 23 - 76 = extracellular  
residues 77 - 99 = transmembrane  
residues 100 - 118 = intracellular  
residues 119 - 141 = transmembrane  
residues 142 - 160 = extracellular  
residues 161 - 183 = transmembrane  
residues 184 - 211 = intracellular

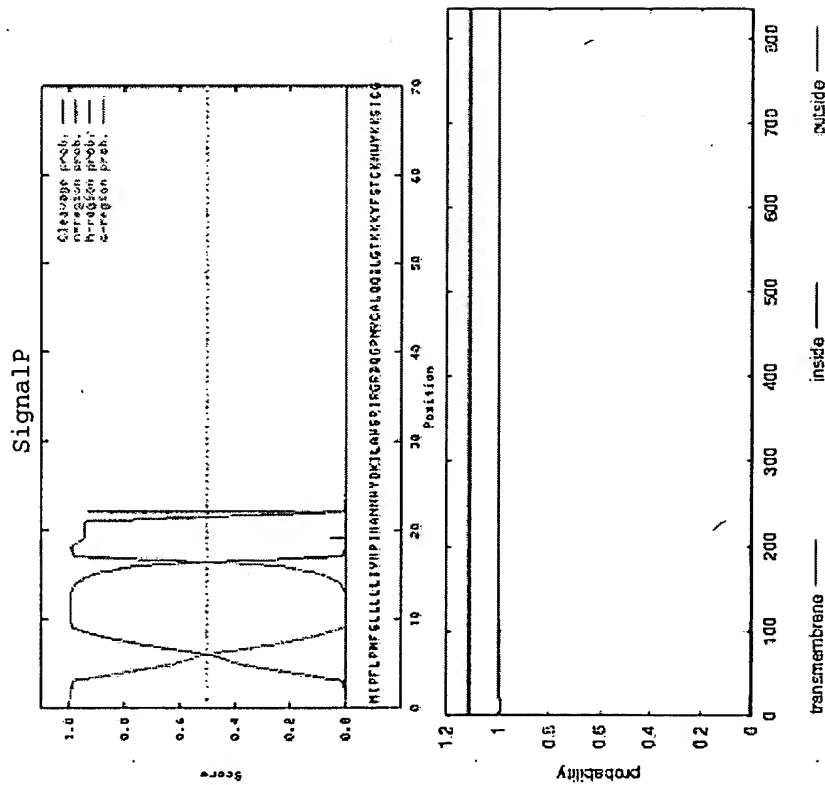


signal peptide probability = 97.6%  
maximum cleavage site probability = 31.4%  
number of probable transmembrane regions = 4  
(#1 cleaved)

Figure 22

PCTUC991 836 amino acids

ANALYSIS  
 Cleaved signal peptide  
 Cleavage site = between position 21 and 22  
 MIPFLPMFSLLLLLLIIVNPINA ↓ NNHYDKILAH...  
 Topology  
 \*SECRETED\*  
 residues 22 - 836 = extracellular



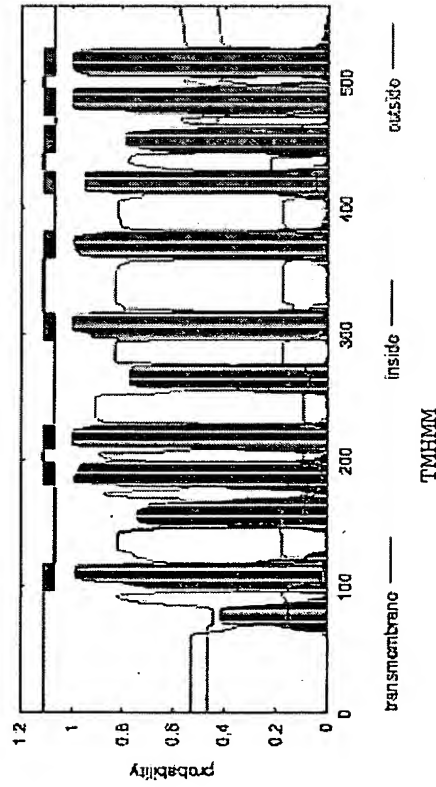
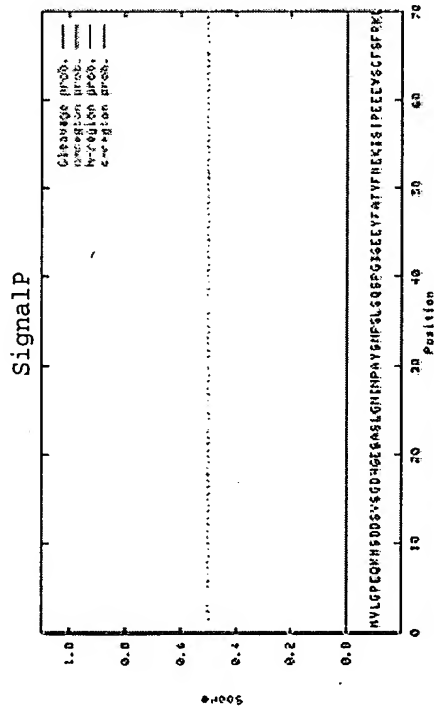
TMHMM

RESULTS

signal peptide probability = 99.9%  
 maximum cleavage site probability = 93.4%  
 number of probable transmembrane regions = 0

Figure 23

PCTUC992 561 amino acids



RESULTS

signal peptide probability = 0%

signal anchor probability = 0%

number of probable transmembrane regions = 9

ANALYSIS

N-terminal signal sequence independent membrane insertion

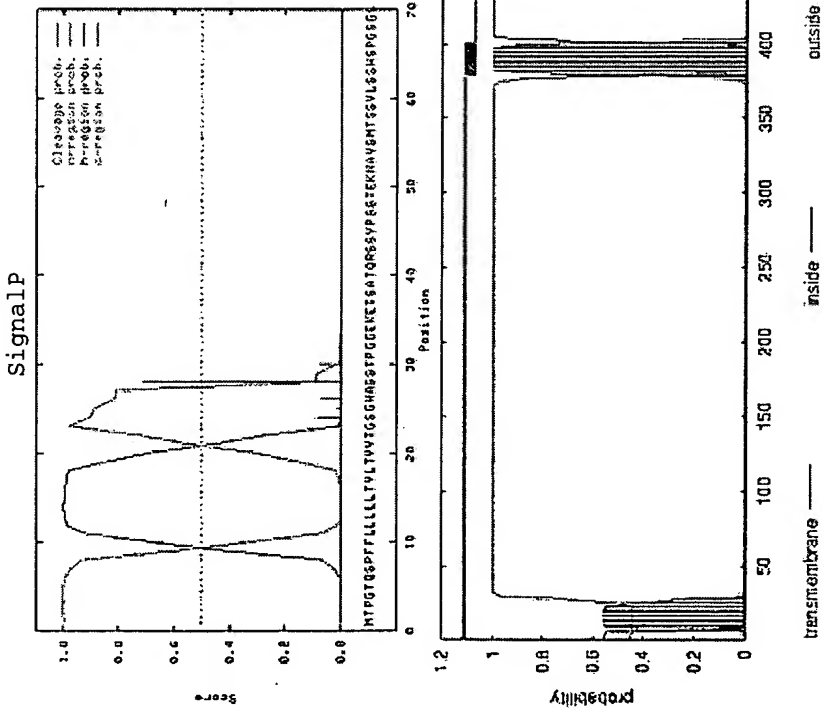
Topology

N-terminus external & C-terminus internal

residues 1 - 95 = extracellular
residues 96 - 118 = transmembrane
residues 119 - 179 = intracellular
residues 180 - 199 = transmembrane
residues 200 - 208 = extracellular
residues 209 - 228 = transmembrane
residues 229 - 294 = intracellular
residues 295 - 317 = transmembrane
residues 318 - 359 = extracellular
residues 360 - 382 = transmembrane
residues 383 - 411 = intracellular
residues 412 - 429 = transmembrane
residues 430 - 443 = extracellular
residues 444 - 466 = transmembrane
residues 467 - 472 = intracellular
residues 473 - 495 = transmembrane
residues 496 - 504 = extracellular
residues 505 - 527 = transmembrane
residues 528 - 561 = intracellular

Figure 24

PCTUC1054 475 amino acids



ANALYSIS  
Cleaved signal peptide  
Cleavage site = between position 27 and 28  
MTPGTQSPFFLLLLLTVLTVVTGSGHA ↓ SSTPGGEKET...  
Topology

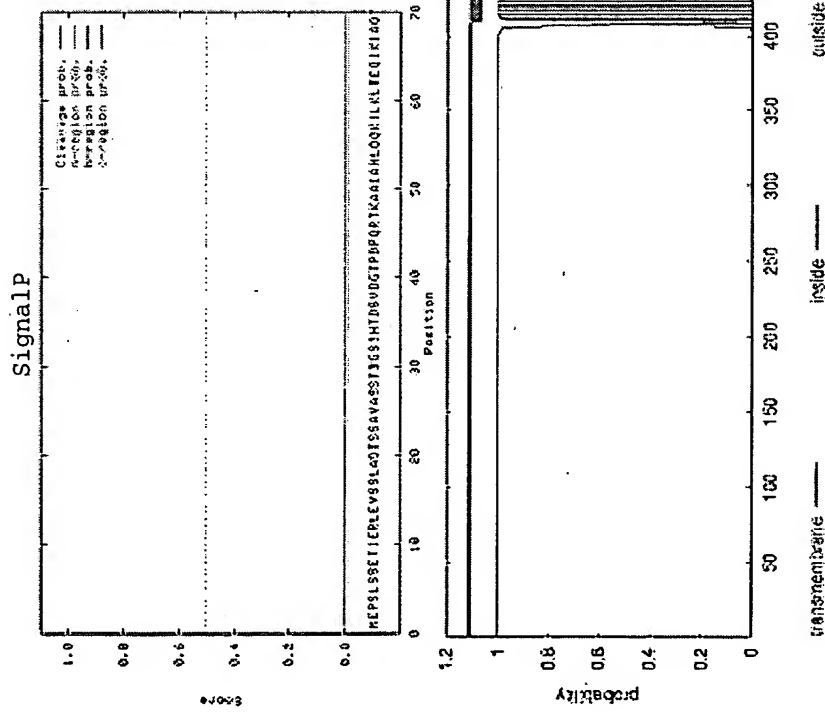
N-terminus external & C-terminus internal  
residues 28 - 378 = extracellular  
residues 379 - 401 = transmembrane  
residues 402 - 475 = intracellular

RESULTS  
signal peptide probability = 99.8%  
maximum cleavage site probability = 71.4%  
number of probable transmembrane regions = 1



**Figure 25**

**PCTUC1061 470 amino acids**



# ANALYSIS

N-terminal signal sequence independent membrane insertion

## Topology

N-terminus & C-terminus external  
 residues 1 - 408 = extracellular  
 residues 409 - 431 = transmembrane  
 residues 432 - 437 = intracellular  
 residues 438 - 455 = transmembrane  
 residues 456 - 470 = extracellular

## RESULTS

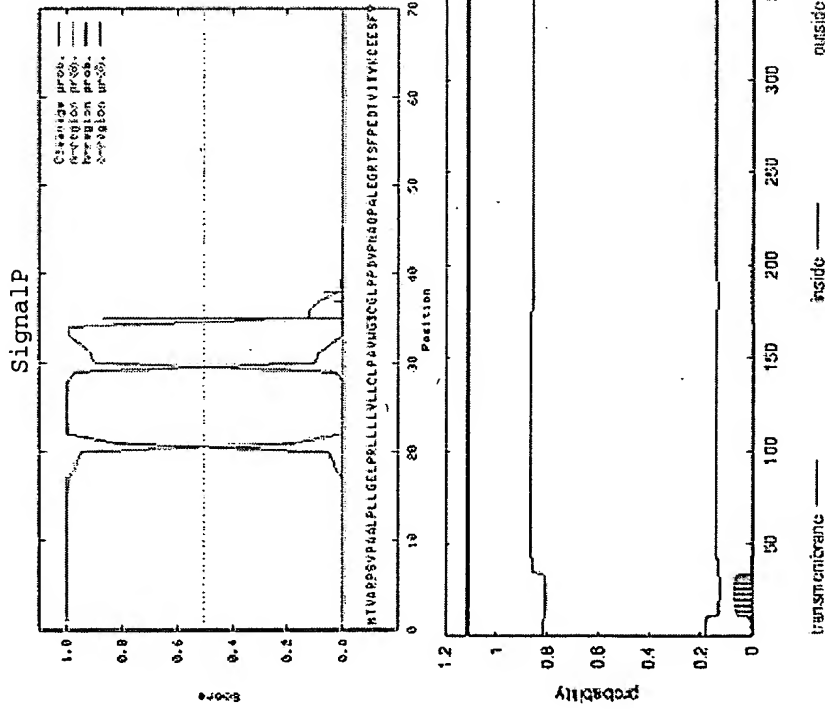
signal peptide probability = 0.6%

signal anchor probability = 0.1%

number of probable transmembrane regions = 2

Figure 26

PCTUC1073 381 amino acids



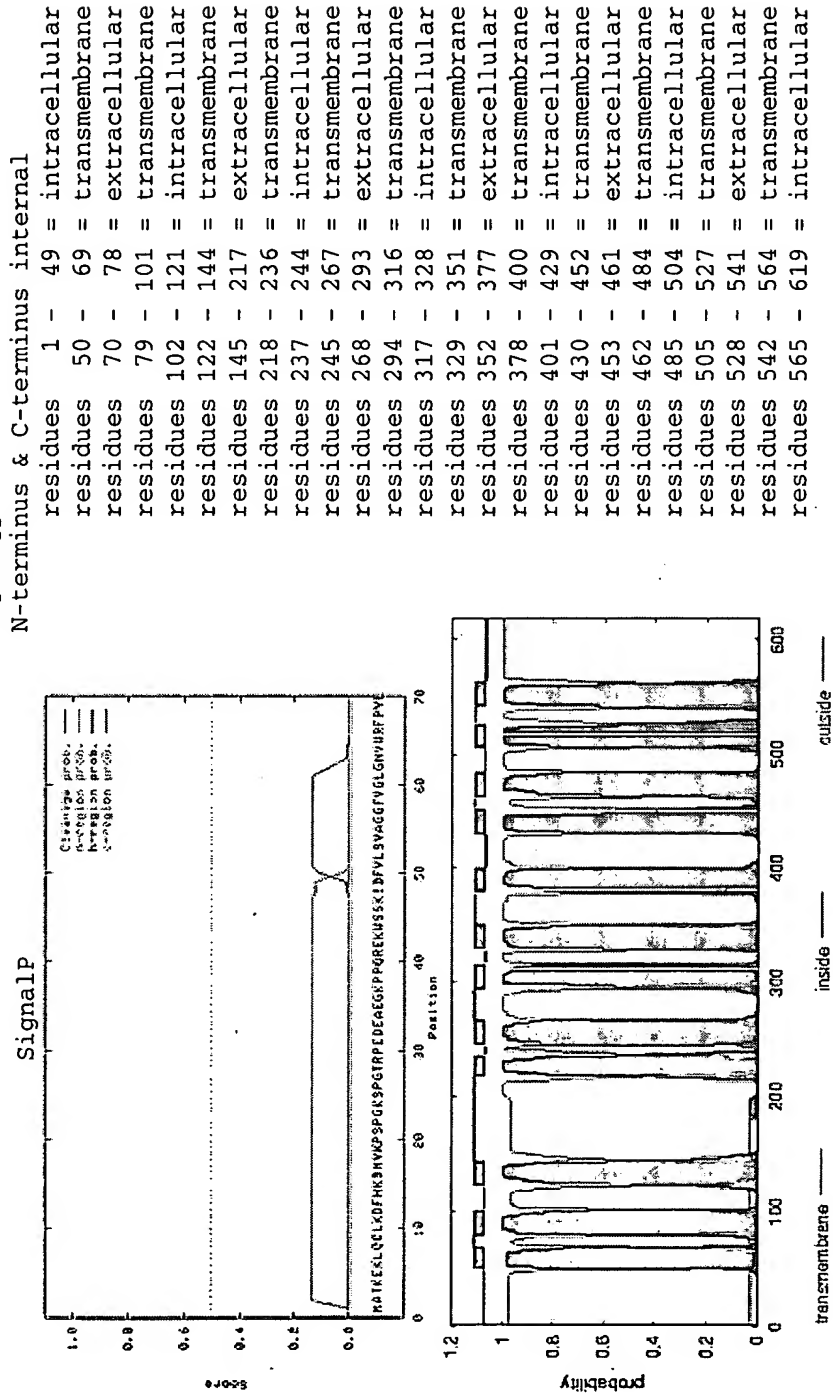
ANALYSIS  
Cleaved signal peptide  
Cleavage site = between position 34 and 35  
MTVARPSVPAALPLLGLPRLLLVLLCLPAVWG ↓  
DCGLPPDPVN...  
Topology  
\*SECRETED\*  
residues 35 - 381 = extracellular

RESULTS  
signal peptide probability > 99.9%  
maximum cleavage site probability = 86.9%  
number of probable transmembrane regions = 0

TMHMM

Figure 27

PCTUC1075 619 amino acids



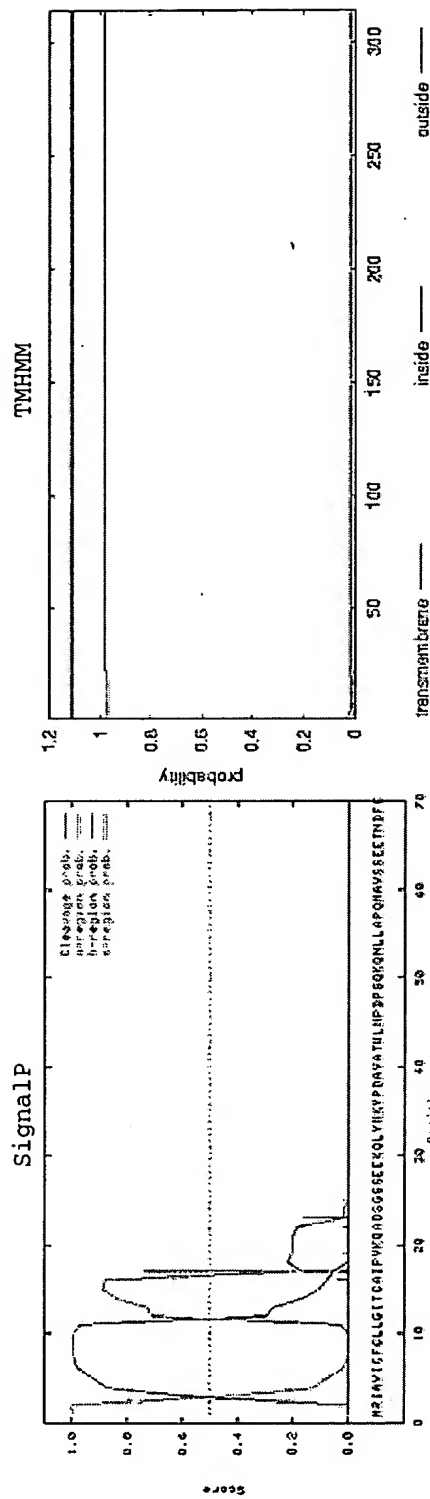
RESULTS

signal peptide probability = 0%  
signal anchor probability = 13.9%  
number of probable transmembrane regions = 12

Figure 28

PCTUC1078

314 amino acids



# RESULTS

signal peptide probability = 99.9%  
 maximum cleavage site probability = 73.6%  
 number of probable transmembrane regions = 0

## ANALYSIS

Cleaved signal peptide

Cleavage site = between position 16 and 17

MRIAVICFLLGITCA ↓ IPVQADSGS...

Topology

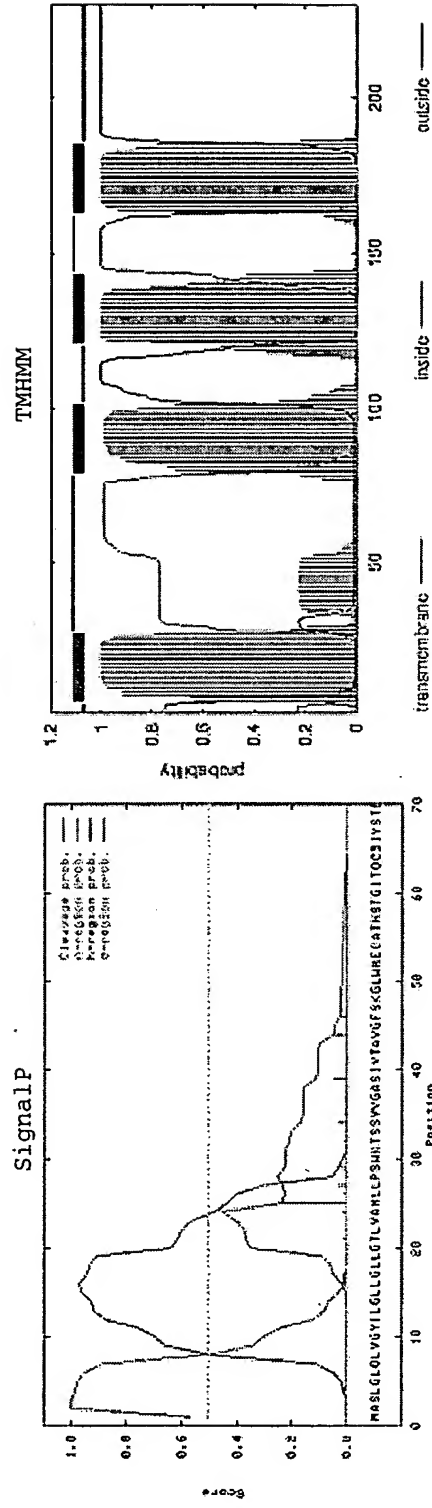
\*SECRETED\*

residues 18 - 314 = extracellular

Figure 29

PCTUC1082

230 amino acids



signal peptide probability = 57.0%  
 maximum cleavage site probability = 23.7%  
 number of probable transmembrane regions = 4 (#1 cleaved)

#### ANALYSIS

Cleaved signal peptide

Cleavage site = between position 24 and 25

MASLGLVGVYILGLLGLTVA ↓ MLLPSWKTSS...

#### Topology

N-terminus external & C-terminus internal

residues 25 - 78 = extracellular

residues 79 - 101 = transmembrane

residues 102 - 120 = intracellular

residues 121 - 143 = transmembrane

residues 144 - 162 = extracellular

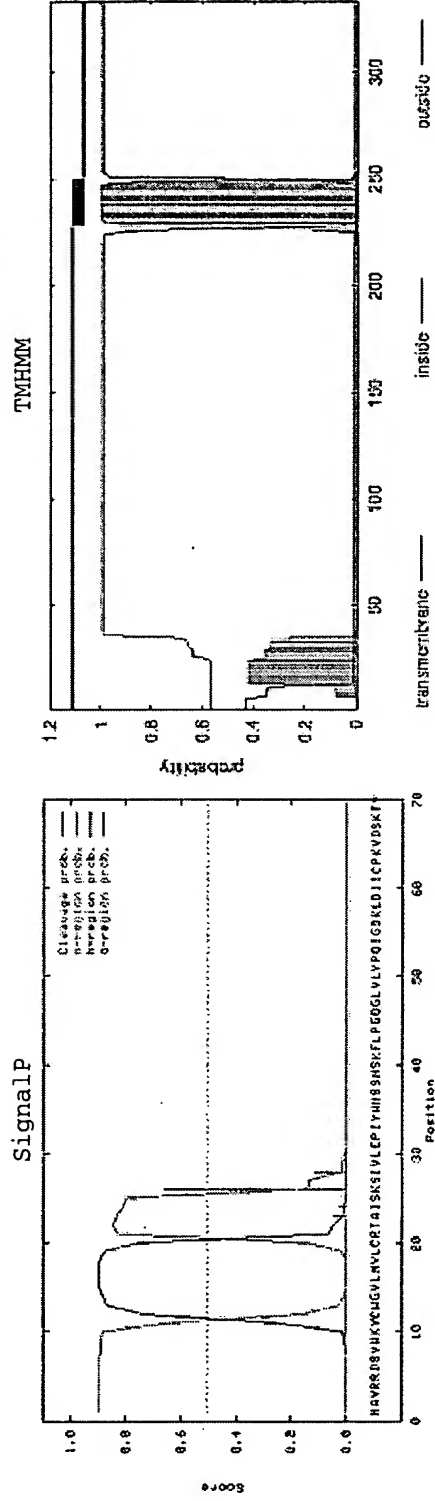
residues 163 - 185 = transmembrane

residues 186 - 230 = intracellular

Figure 30

PCTUC1122

333 amino acids



## RESULTS

signal peptide probability = 89.5%  
 maximum cleavage site probability = 65.9%  
 number of probable transmembrane regions = 1

## ANALYSIS

Cleaved signal peptide

Cleavage site = between position 25 and 26

MAVRDSDVWKYCWGVLMLCRTAIS ↓ KSIVLEPIYW...

## Topology

N-terminus external & C-terminus internal

residues 26 - 227 = extracellular

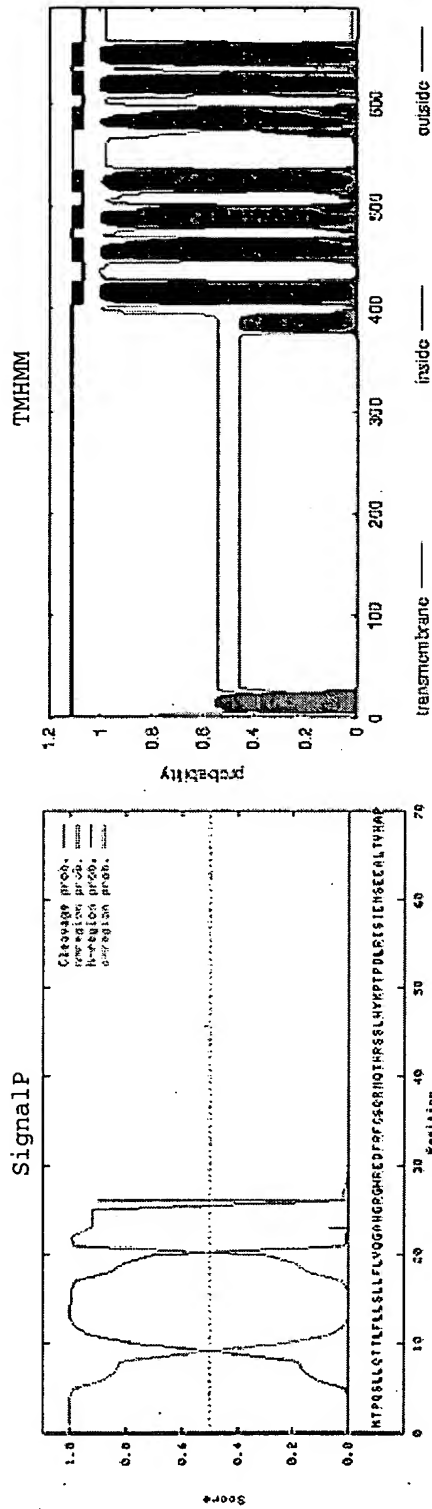
residues 228 - 250 = transmembrane

residues 251 - 333 = intracellular

Figure 31

PCTUC250

693 amino acids



## RESULTS

signal peptide probability > 99.9%  
 maximum cleavage site probability = 90.4%  
 number of probable transmembrane regions = 7

## ANALYSIS

Cleaved signal peptide

Cleavage site = between position 25 and 26

MTPQSLQTTLLFLSLFLVQGAHG ↓ RGHREDFRFC

Topology

N-terminus external & C-terminus internal

residues 26 - 404 = extracellular

residues 405 - 427 = transmembrane

residues 428 - 446 = intracellular

residues 447 - 469 = transmembrane

residues 470 - 478 = extracellular

residues 479 - 501 = transmembrane

residues 502 - 513 = intracellular

residues 514 - 536 = transmembrane

residues 537 - 574 = extracellular

residues 575 - 597 = transmembrane

residues 598 - 608 = intracellular

residues 609 - 631 = transmembrane

residues 632 - 636 = extracellular

residues 637 - 659 = transmembrane

residues 660 - 693 = intracellular